

<220>

<221> PEPTIDE
 <222> (9)
 <223> Xaa at residue 9 is a peptide having 3-4 amino acids.

<220>
 <221> PEPTIDE
 <222> (11)
 <223> Xaa at residue 11 is a peptide having 3-6 amino acids.

<220>
 <221> PEPTIDE
 <222> (13)
 <223> Xaa at residue 13 is des-Xaa or a peptide of 2-9 amino acids.

<400> 1
 Xaa Cys Xaa Cys Xaa Xaa Cys Cys Xaa Cys Xaa Cys Xaa
 1 5 10

<210> 2
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:generic sequence of gamma-conopeptides.

<220>
 <221> PEPTIDE
 <222> (1)
 <223> Xaa at residue 1 is des-Xaa or a peptide having 1-6 amino acids.

<220>
 <221> PEPTIDE
 <222> (3)
 <223> Xaa at residue 3 is a peptide having 5-6 amino acids.

<220>
 <221> PEPTIDE
 <222> (5)
 <223> Xaa at residue 5 is a peptide having 4 amino acids.

<220>
 <221> PEPTIDE
 <222> (6)
 <223> Xaa at residue 6 is Glu, gamma-carboxyglutamate or Gln.

<220>
 <221> PEPTIDE
 <222> (9)
 <223> Xaa at residue 9 is Ser or Thr.

<220>
 <221> PEPTIDE
 <222> (10)
 <223> Xaa at residue 10 is a peptide having 2-3 amino

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acids.

<220>
 <221> PEPTIDE
 <222> (12)
 <223> Xaa at residue 12 is a peptide having 3-6 amino acids.

<220>
 <221> PEPTIDE
 <222> (14)
 <223> Xaa at residue 14 is a peptide having 2-9 amino acids.

<400> 2
 Xaa Cys Xaa Cys Xaa Xaa Cys Cys Xaa Xaa Cys Xaa Cys Xaa
 1 5 10

<210> 3
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:generic formula of gamma-conopeptides

<220>
 <221> PEPTIDE
 <222> (1)
 <223> Xaa at residue 1 is a peptide having 1-6 amino acids.

<220>
 <221> PEPTIDE
 <222> (3)
 <223> Xaa at residue 3 is a hexapeptide.

<220>
 <221> PEPTIDE
 <222> (5)
 <223> Xaa at residue 5 is a peptide having 4 amino acids.

<220>
 <221> PEPTIDE
 <222> (6)
 <223> Xaa at residue 6 is Glu or gamma-carboxyglutamate.

<220>
 <221> PEPTIDE
 <222> (14)
 <223> Xaa at residue 14 is a tripeptide.

<220>
 <221> PEPTIDE
 <222> (16)
 <223> Xaa at residue 16 is a peptide having 7-9 amino acids.

<400> 3
 Xaa Cys Xaa Cys Xaa Xaa Cys Cys Ser Asn Ser Cys Asp Xaa Cys Xaa
 1 5 10 15

001095.1450

<210> 4
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:generic
 sequence of gamma-conopeptides.

<220>
 <221> PEPTIDE
 <222> (1)
 <223> Xaa at residue 1 is a peptide having 1-6 amino
 acids.

<220>
 <221> PEPTIDE
 <222> (3)
 <223> Xaa at residue 3 is a hexapeptide.

<220>
 <221> PEPTIDE
 <222> (5)
 <223> Xaa at residue 5 is Ser or Thr.

<220>
 <221> PEPTIDE
 <222> (6)
 <223> Xaa at residue 6 is a tripeptide.

<220>
 <221> PEPTIDE
 <222> (7)
 <223> Xaa at residue 7 is Glu or gamma-carboxyglutamate.

<220>
 <221> PEPTIDE
 <222> (15)
 <223> Xaa at residue 15 is a tripeptide.

<220>
 <221> PEPTIDE
 <222> (17)
 <223> Xaa at residue is a peptide having 7-9 amino
 acids.

<400> 4
 Xaa Cys Xaa Cys Xaa Xaa Xaa Cys Cys Ser Asn Ser Cys Asp Xaa Cys
 1 5 10 15

Xaa

<210> 5
 <211> 26
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:generic
 sequence of gamma-conopeptides.

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<220>
 <221> PEPTIDE
 <222> (1)
 <223> Xaa at residue 1 is des-Xaa or a dipeptide.

<220>
 <221> PEPTIDE
 <222> (2)
 <223> Xaa at residue 2 is Asp, Glu or
 gamma-carboxyglutamate.

<220>
 <221> PEPTIDE
 <222> (4)
 <223> Xaa at residue 4 is a dipeptide.

<220>
 <221> PEPTIDE
 <222> (5)
 <223> Xaa at residue 5 is Trp or 6-bromo-Trp.

<220>
 <221> PEPTIDE
 <222> (7)
 <223> Xaa at residue 7 is dipeptide.

<220>
 <221> PEPTIDE
 <222> (10)
 <223> Xaa at residue 10 is a dipeptide.

<220>
 <221> PEPTIDE
 <222> (12)
 <223> Xaa at residue 12 is Glu, gamma-carboxyglutamate
 or Gln.

<220>
 <221> PEPTIDE
 <222> (24)
 <223> Xaa at residue 24 is any amino acid.

<220>
 <221> PEPTIDE
 <222> (26)
 <223> Xaa at residue 26 is a pentapeptide.

<400> 5
 Xaa Xaa Cys Xaa Xaa Phe Xaa Cys Thr Xaa Ser Xaa Cys Cys Ser Asn
 1 5 10 15

Ser Cys Asp Trp Thr Tyr Cys Xaa Leu Xaa
 20 25

<210> 6
 <211> 32
 <212> PRT
 <213> Conus pennaceus

<220>
 <221> PEPTIDE
 <222> (1)..(31)
 <223> Xaa at residue 5 is Trp or 6-bromo-Trp; Xaa at

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residues 14 and 26 are Glu or
gamma-carboxyglutamate; Xaa at residue 31 is Pro
or hydroxy-Pro.

<400> 6
Asp Cys Thr Ser Xaa Phe Gly Arg Cys Thr Val Asn Ser Xaa Cys Cys
1 5 10 15
Ser Asn Ser Cys Asp Gln Thr Tyr Cys Xaa Leu Tyr Ala Phe Xaa Ser
20 25 30

<210> 7
<211> 34
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(34)
<223> Xaa at residues 1, 7 and 34 are Trp or
6-bromo-Trp; Xaa at residues 3 and 16 are Glu or
gamma-carboxyglutamate; Xaa at residues 31 and 32
are Pro or hydroxy-Pro.

<400> 7
Xaa Leu Xaa Cys Ser Val Xaa Phe Ser His Cys Thr Lys Asp Ser Xaa
1 5 10 15
Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Thr Leu Met Xaa Xaa
20 25 30
Asp Xaa

<210> 8
<211> 39
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(39)
<223> Xaa at residues 1, 2, 4, 10 and 39 are Trp or
6-bromo-Trp ; Xaa at residues 19 and 31 are Glu or
gamma-carboxyglutamate; Xaa at residues 34, 36 and
37 are Pro or hydroxy-Pro.

<400> 8
Xaa Xaa Arg Xaa Gly Gly Cys Met Ala Xaa Phe Gly Leu Cys Ser Arg
1 5 10 15
Asp Ser Xaa Cys Cys Ser Asn Ser Cys Asp Val Thr Arg Cys Xaa Leu
20 25 30
Met Xaa Phe Xaa Xaa Asp Xaa
35

<210> 9

0021052.12158

<211> 27
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa at residues 9, 13 and 17 are Glu or
gamma-carboxyglutamate.

<400> 9
Cys Lys Thr Tyr Ser Lys Tyr Cys Xaa Ala Asp Ser Xaa Cys Cys Thr
1 5 10 15

Xaa Gln Cys Val Arg Ser Tyr Cys Thr Leu Phe
20 25

<210> 10
<211> 34
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(34)
<223> Xaa at residues 2, 3, 10 and 32 are Trp or
6-bromo-Trp; Xaa at residues 18, 26 and 33 are Glu
or gamma-carboxyglutamate; Xaa at residue 12 is
Pro or hydroxy-Pro.

<400> 10
Asp Xaa Xaa Asp Asp Gly Cys Ser Val Xaa Gly Xaa Cys Thr Tyr Asn
1 5 10 15

Ala Xaa Cys Cys Ser Gly Asp Cys His Xaa Thr Cys Ile Phe Gly Xaa
20 25 30

Xaa Val

<210> 11
<211> 31
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(31)
<223> Xaa at residues 3 and 31 are Trp of 6-bromo-Trp;
Xaa at residues 5, 18, 22 and 25 are Glu or
gamma-carboxyglutamate; Xaa at residue 16 is Pro
or hydroxy-Pro.

<400> 11
Gly Met Xaa Gly Xaa Cys Lys Asp Gly Leu Thr Thr Cys Leu Ala Xaa
1 5 10 15

Ser Xaa Cys Cys Ser Xaa Asp Cys Xaa Gly Ser Cys Thr Met Xaa
20 25 30

<210> 12

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<211> 32
<212> PRT
<213> Conus gloriamaris

<220>
<221> PEPTIDE
<222> (1)..(32)
<223> Xaa at residue 5 is Trp or 6-bromo-Trp; Xaa at residue 1 is Glu or gamma-carboxyglutamate; Xaa at residues 8 and 11 are Pro or hydroxy-Pro.

<400> 12
Xaa Cys Arg Ala Xaa Tyr Ala Xaa Cys Ser Xaa Gly Ala Gln Cys Cys
1 5 10 15
Ser Leu Leu Met Cys Ser Lys Ala Thr Ser Arg Cys Ile Leu Ala Leu
20 25 30

<210> 13
<211> 29
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(29)
<223> Xaa at residues 8 and 15 are Trp or 6-bromo-Trp; Xaa at residues 5, 16 and 23 are Glu or gamma-carboxyglutamate; Xaa at residue 10 is Pro or hydroxy-Pro.

<400> 13
Asn Gly Gln Cys Xaa Asp Val Xaa Met Xaa Cys Thr Ser Asn Xaa Xaa
1 5 10 15
Cys Cys Ser Leu Asp Cys Xaa Met Tyr Cys Thr Gln Ile
20 25

<210> 14
<211> 27
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa at residue 4 is Trp or 6-bromo-Trp; Xaa at residues 9, 12, 13 and 17 are Glu or gamma-carboxyglutamate.

<400> 14
Cys Gly Gly Xaa Ser Thr Tyr Cys Xaa Val Asp Xaa Xaa Cys Cys Ser
1 5 10 15
Xaa Ser Cys Val Arg Ser Tyr Cys Thr Leu Phe
20 25

<210> 15

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<211> 26
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(26)
<223> Xaa at residues 8 and 15 are Trp or 6-bromo-Trp;
Xaa at residue 16 is Glu or
gamma-carboxyglutamate.

<400> 15
Asn Gly Gly Cys Lys Ala Thr Xaa Met Ser Cys Ser Ser Gly Xaa Xaa
1 5 10 15
Cys Cys Ser Met Ser Cys Asp Met Tyr Cys
20 25

<210> 16
<211> 323
<212> DNA
<213> Conus textile

<220>
<221> CDS
<222> (1)..(153)

<400> 16
gaa cgg gct aag atc aac ttg ctt cca aag aga aag cca cct gct gag 48
Glu Arg Ala Lys Ile Asn Leu Leu Pro Lys Arg Lys Pro Pro Ala Glu
1 5 10 15
cgt tgg ttg gaa tgc agt gtt tgg ttt tca cat tgt acg aag gac tcg 96
Arg Trp Leu Glu Cys Ser Val Trp Phe Ser His Cys Thr Lys Asp Ser
20 25 30
gaa tgt tgt tct aat agt tgt gac caa acg tac tgc acg tta atg cca 144
Glu Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Thr Leu Met Pro
35 40 45
ccg gac tgg tgacatcgcc actctcctgt tcagagtctt caaggctttt 193
Pro Asp Trp
50
gttctctttt gaagaatttt aacgagtga caaaaaagt gactagcatg tttccttttc 253
cctttgcaaa atcaatgatg gaggtaaaag cctcccat tgtcttcac aataaagaac 313
ttatcatcat 323

<210> 17
<211> 51
<212> PRT
<213> Conus textile

<400> 17
Glu Arg Ala Lys Ile Asn Leu Leu Pro Lys Arg Lys Pro Pro Ala Glu
1 5 10 15
Arg Trp Leu Glu Cys Ser Val Trp Phe Ser His Cys Thr Lys Asp Ser
20 25 30

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Glu Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Thr Leu Met Pro
35 40 45

Pro Asp Trp
50

<210> 18
<211> 510
<212> DNA
<213> Conus textile

<220>
<221> CDS
<222> (95)..(337)

<400> 18
tgactcgcca tctcctctct cagtctccct gacagctgcc ttcagtcgac cctgccgtca 60
tctcaacgca cacttgaagt gaaaaacctt tate atg gag aaa ctg aca att ctg 115
Met Glu Lys Leu Thr Ile Leu
1 5

ctt ctt gtt gct gct gta ctg ttg tgg atc cag gcc cta aat caa gaa 163
Leu Leu Val Ala Ala Val Leu Leu Ser Ile Gln Ala Leu Asn Gln Glu
10 15 20

aaa cac caa cgg gca aag atc aac ttg ctt tca aag aga aag cca cct 211
Lys His Gln Arg Ala Lys Ile Asn Leu Leu Ser Lys Arg Lys Pro Pro
25 30 35

gct gag cgt tgg tgg cgg tgg gga gga tgc atg gct tgg ttt ggg ctt 259
Ala Glu Arg Trp Trp Arg Trp Gly Gly Cys Met Ala Trp Phe Gly Leu
40 45 50 55

tgt tgg agg gac tgg gaa tgt tgt tct aat agt tgt gac gta acg cgc 307
Cys Ser Arg Asp Ser Glu Cys Cys Ser Asn Ser Cys Asp Val Thr Arg
60 65 70

tgc gag tta atg cca ttc cca cca gac tgg tgacatcgac actctcctct 357
Cys Glu Leu Met Pro Phe Pro Pro Asp Trp
75 80

tcagagtctt caaggctttt gttctctttt gaagaatttt tacgagtga caaaaacgtg 417
gactagcacg tttccttttc cctttgcaaa atcaatgatg gaggtaaaag tgtcccattt 477
tgtcttcac cataaagaac ttatcatcat aat 510

<210> 19
<211> 81
<212> PRT
<213> Conus textile

<400> 19
Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Leu Ser
1 5 10 15
Ile Gln Ala Leu Asn Gln Glu Lys His Gln Arg Ala Lys Ile Asn Leu
20 25 30
Leu Ser Lys Arg Lys Pro Pro Ala Glu Arg Trp Trp Arg Trp Gly Gly
35 40 45

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Cys Met Ala Trp Phe Gly Leu Cys Ser Arg Asp Ser Glu Cys Cys Ser
50 55 60

Asn Ser Cys Asp Val Thr Arg Cys Glu Leu Met Pro Phe Pro Pro Asp
65 70 75 80

Trp

<210> 20
<211> 441
<212> DNA
<213> Conus textile

<220>
<221> CDS
<222> (16)..(243)

<400> 20
ggaaaaactt ttatc atg gag aaa ctg aca atc ctg ctc ctt gtt gct gct 51
Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala
1 5 10
gta ctg atg tgc acc cag gcc atg ttt caa ggt gat gga gaa aaa tcc 99
Val Leu Met Ser Thr Gln Ala Met Phe Gln Gly Asp Gly Glu Lys Ser
15 20 25
cgg aag gcg gag atc aac ttt tct gaa aca aga aag ttg gcg aga aac 147
Arg Lys Ala Glu Ile Asn Phe Ser Glu Thr Arg Lys Leu Ala Arg Asn
30 35 40
aag cag aaa ggc tgc aaa act tat tca aag tat tgt gaa gct gac tgc 195
Lys Gln Lys Arg Cys Lys Thr Tyr Ser Lys Tyr Cys Glu Ala Asp Ser
45 50 55 60
gaa tgc tgt acc gaa cag tgt gta agg tct tac tgc acg ttg ttt gga 243
Glu Cys Cys Thr Glu Gln Cys Val Arg Ser Tyr Cys Thr Leu Phe Gly
65 70 75
tgaattcgga ccacaagcca tccgatatca cccctctcct cttcagaggc ttcaaggctt 303
ttgttatcct tttgaagaat ctttatcgag taaacataag tagacaagct ttttttttcc 363
tttgcaaaat gaagaatgat ggcaaaaagc cccccatttt gtcttcatca ataaagaact 423
cgctatcaga ataaaaaa 441

<210> 21
<211> 76
<212> PRT
<213> Conus textile

<400> 21
Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser
1 5 10 15
Thr Gln Ala Met Phe Gln Gly Asp Gly Glu Lys Ser Arg Lys Ala Glu
20 25 30
Ile Asn Phe Ser Glu Thr Arg Lys Leu Ala Arg Asn Lys Gln Lys Arg
35 40 45

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Cys Lys Thr Tyr Ser Lys Tyr Cys Glu Ala Asp Ser Glu Cys Cys Thr
50 55 60

Glu Gln Cys Val Arg Ser Tyr Cys Thr Leu Phe Gly
65 70 75

<210> 22
<211> 460
<212> DNA
<213> Conus textile

<220>
<221> CDS
<222> (49)..(273)

<400> 22
ctgccgtcat ctcagcgcac acttggttaag aagtgaaaaa ccttgatc atg gag aaa 57
Met Glu Lys
1

ctg aca att ctg ctt ctt gtt gct gct gtg ctg atg tcg acc cag gcc 105
Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala
5 10 15

cta att caa gat caa cgc caa aag gca aag atc aac ttg ttt tca aag 153
Leu Ile Gln Asp Gln Arg Gln Lys Ala Lys Ile Asn Leu Phe Ser Lys
20 25 30 35

aga cag gca tat gct cgt gat tgg tgg gac gat ggc tgc agt gtg tgg 201
Arg Gln Ala Tyr Ala Arg Asp Trp Trp Asp Asp Gly Cys Ser Val Trp
40 45 50

ggg cct tgt acg gtg aac gca gaa tgt tgt tct ggt gat tgt cat gaa 249
Gly Pro Cys Thr Val Asn Ala Glu Cys Cys Ser Gly Asp Cys His Glu
55 60 65

acg tgc att ttc ggg tgg gaa gtc tgaccacaaa ccatccgaca tcgccactct 303
Thr Cys Ile Phe Gly Trp Glu Val
70 75

cctcttcaga gacttcaagg cttttgttct cttttgaaga attttacgag tgagcaaaaa 363

ggtagactag cacgtttctt tttcccttg caaatcaat gatggaggta aaagcctccc 423

atthttgtcct catcaataaa gaacttatca tcataat 460

<210> 23
<211> 75
<212> PRT
<213> Conus textile

<400> 23
Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser
1 5 10 15

Thr Gln Ala Leu Ile Gln Asp Gln Arg Gln Lys Ala Lys Ile Asn Leu
20 25 30

Phe Ser Lys Arg Gln Ala Tyr Ala Arg Asp Trp Trp Asp Asp Gly Cys
35 40 45

Ser Val Trp Gly Pro Cys Thr Val Asn Ala Glu Cys Cys Ser Gly Asp

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50

55

60

Cys His Glu Thr Cys Ile Phe Gly Trp Glu Val
65 70 75

<210> 24
<211> 533
<212> DNA
<213> Conus textile

<220>
<221> CDS
<222> (110)..(337)

<400> 24
ctctgccggt tgacacntca tctactctct cagtctccct gacagctgcc ttcagtcgac 60
cctgccgtca tctcagcgca gacttgataa gaagtgaata acctttatc atg gag aaa 118
Met Glu Lys
1

ctg aca atc ctg ctt ctt gtt gct gct gta ctg atg tcg acc cag gcc 166
Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala
5 10 15

ctg gtt gaa cgt gct gga gaa aac cac tca aag gag aac atc aat ttt 214
Leu Val Glu Arg Ala Gly Glu Asn His Ser Lys Glu Asn Ile Asn Phe
20 25 30 35

tta tta aaa aga aag aga gct gct gac agg ggg atg tgg ggc gaa tgc 262
Leu Leu Lys Arg Lys Arg Ala Ala Asp Arg Gly Met Trp Gly Glu Cys
40 45 50

aaa gat ggg tta acg aca tgt ttg gcg ccc tca gag tgt tgt tct gag 310
Lys Asp Gly Leu Thr Thr Cys Leu Ala Pro Ser Glu Cys Cys Ser Glu
55 60 65

gat tgt gaa ggg agc tgc acg atg tgg tgatgaattc tgaccacaag 357
Asp Cys Glu Gly Ser Cys Thr Met Trp
70 75

ccatctgaca tcaccactct cctcttcaga ggcttcaagg cttttgtttt ctttttgaat 417

aatctttacg agtaaacaaa taagtagact agcgogtttt tttccctttg agaaatcaat 477

gatggaggta aatagcttcc tattttgtct tattcaataa agaacttatc ataata 533

<210> 25
<211> 76
<212> PRT
<213> Conus textile

<400> 25
Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser
1 5 10 15

Thr Gln Ala Leu Val Glu Arg Ala Gly Glu Asn His Ser Lys Glu Asn
20 25 30

Ile Asn Phe Leu Leu Lys Arg Lys Arg Ala Ala Asp Arg Gly Met Trp
35 40 45

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Gly Glu Cys Lys Asp Gly Leu Thr Thr Cys Leu Ala Pro Ser Glu Cys
50 55 60

Cys Ser Glu Asp Cys Glu Gly Ser Cys Thr Met Trp
65 70 75

<210> 26
<211> 408
<212> DNA
<213> Conus gloriamaris

<220>
<221> CDS
<222> (2)..(211)

<400> 26
g ctg aca atc ctg ctt ctt gtt gct gct gta ctg atg tcg acc cag gcc 49
Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala
1 5 10 15

ctg att caa ggt ggt ggt gac aaa cgt caa aag gca aac atc aac ttt 97
Leu Ile Gln Gly Gly Gly Asp Lys Arg Gln Lys Ala Asn Ile Asn Phe
20 25 30

ctt tca agg tgg gac cgt gag tgc agg gct tgg tat gcg ccg tgt agc 145
Leu Ser Arg Trp Asp Arg Glu Cys Arg Ala Trp Tyr Ala Pro Cys Ser
35 40 45

cct ggc gcg caa tgt tgt agt ttg ctg atg tgt tca aaa gcg acc agc 193
Pro Gly Ala Gln Cys Cys Ser Leu Leu Met Cys Ser Lys Ala Thr Ser
50 55 60

cgc tgc ata ttg gcg tta tgaactctga ccacaagcca tccgacatca 241
Arg Cys Ile Leu Ala Leu
65 70

ccactctcct cttcagaggc ttcaaggctt tttgtttttc ttttgaagaa tctttacgag 301

tgaacaaata agtagaatag cacgtttttc cccctttgca aaatcaataa tggagggttaa 361

aaaaaaaactt ctgtcttctt caataaagaa gttatcataa taaaaaa 408

<210> 27
<211> 70
<212> PRT
<213> Conus gloriamaris

<400> 27
Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala
1 5 10 15

Leu Ile Gln Gly Gly Gly Asp Lys Arg Gln Lys Ala Asn Ile Asn Phe
20 25 30

Leu Ser Arg Trp Asp Arg Glu Cys Arg Ala Trp Tyr Ala Pro Cys Ser
35 40 45

Pro Gly Ala Gln Cys Cys Ser Leu Leu Met Cys Ser Lys Ala Thr Ser
50 55 60

Arg Cys Ile Leu Ala Leu
65 70

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<210> 28
 <211> 278
 <212> DNA
 <213> Conus marmoreus

<220>
 <221> CDS
 <222> (4)..(222)

<400> 28
 atc atg cag aaa ctg ata atc ctg ctt ctt gtt gct gct gtg ctg ctg 48
 Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Leu 15
 1 5 10 15
 tcg acc cag gcc cta aat caa gaa aaa cgc cca aag gag atg atc aat 96
 Ser Thr Gln Ala Leu Asn Gln Glu Lys Arg Pro Lys Glu Met Ile Asn 30
 20 25 30
 ttt tta tca aaa gga aag aca aat gct gag agg cgg aac ggc caa tgc 144
 Phe Leu Ser Lys Gly Lys Thr Asn Ala Glu Arg Arg Asn Gly Gln Cys 45
 35 40 45
 gag gat gtt tgg atg cct tgt aca tcg aac tgg gaa tgc tgt tct ttg 192
 Glu Asp Val Trp Met Pro Cys Thr Ser Asn Trp Glu Cys Cys Ser Leu 60
 50 55 60
 gat tgt gaa atg tac tgc aca cag ata gga tgaactctga ccacaagcca 242
 Asp Cys Glu Met Tyr Cys Thr Gln Ile Gly 70
 65 70
 tccgacatca ccactctcct cttcagagtc ttcaag 278

<210> 29
 <211> 73
 <212> PRT
 <213> Conus marmoreus

<400> 29
 Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Leu Ser 15
 1 5 10 15
 Thr Gln Ala Leu Asn Gln Glu Lys Arg Pro Lys Glu Met Ile Asn Phe 30
 20 25 30
 Leu Ser Lys Gly Lys Thr Asn Ala Glu Arg Arg Asn Gly Gln Cys Glu 45
 35 40 45
 Asp Val Trp Met Pro Cys Thr Ser Asn Trp Glu Cys Cys Ser Leu Asp 60
 50 55 60
 Cys Glu Met Tyr Cys Thr Gln Ile Gly 70
 65 70

<210> 30
 <211> 287
 <212> DNA
 <213> Conus marmoreus

<220>
 <221> CDS
 <222> (4)..(231)

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<400> 30
 atc atg gag aaa ctg aca atc ctg ctt ctt gtt gct gct gta ctg ata 48
 Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Ile
 1 5 10 15

ccg acc cag gcc ctt ttt caa ggt gat gac gga aaa tcc cag aag gcg 96
 Pro Thr Gln Ala Leu Phe Gln Gly Asp Asp Gly Lys Ser Gln Lys Ala
 20 25 30

gag atc aag tct ttt gaa aca aga aag tta gcg aga aac aag cag gta 144
 Glu Ile Lys Ser Phe Glu Thr Arg Lys Leu Ala Arg Asn Lys Gln Val
 35 40 45

cgc tgc ggt ggt tgg tca acg tat tgt gaa gtt gac gag gaa tgc tgt 192
 Arg Cys Gly Gly Trp Ser Thr Tyr Cys Glu Val Asp Glu Glu Cys Cys
 50 55 60

tcg gaa tca tgt gta agg tct tac tgc acg ctg ttt gga tgaactcgga 241
 Ser Glu Ser Cys Val Arg Ser Tyr Cys Thr Leu Phe Gly
 65 70 75

ccacaagcca tccgatatca ccactctcct gttcagagtc ttcaag 287

<210> 31
 <211> 76
 <212> PRT
 <213> Conus marmoreus

<400> 31
 Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Ile Pro
 1 5 10 15

Thr Gln Ala Leu Phe Gln Gly Asp Asp Gly Lys Ser Gln Lys Ala Glu
 20 25 30

Ile Lys Ser Phe Glu Thr Arg Lys Leu Ala Arg Asn Lys Gln Val Arg
 35 40 45

Cys Gly Gly Trp Ser Thr Tyr Cys Glu Val Asp Glu Glu Cys Cys Ser
 50 55 60

Glu Ser Cys Val Arg Ser Tyr Cys Thr Leu Phe Gly
 65 70 75

<210> 32
 <211> 278
 <212> DNA
 <213> Conus marmoreus

<220>
 <221> CDS
 <222> (4)..(213)

<400> 32
 atc atg cag aaa ctg ata att ctg ctt ctt gtt gct gct gtg ctg atg 48
 Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met
 1 5 10 15

acg acc cag gcc cta tat caa gaa aaa cgc cga aag gag atg atc aat 96
 Thr Thr Gln Ala Leu Tyr Gln Glu Lys Arg Arg Lys Glu Met Ile Asn
 20 25 30

0010955125607260

ttt tta tca aaa gga aag ata aat gct gag agg cgg aac ggc gga tgc 144
Phe Leu Ser Lys Gly Lys Ile Asn Ala Glu Arg Arg Asn Gly Gly Cys
35 40 45

aaa gct act tgg atg tct tgt tca tcg ggc tgg gaa tgc tgt tct atg 192
Lys Ala Thr Trp Met Ser Cys Ser Ser Gly Trp Glu Cys Cys Ser Met
50 55 60

agt tgt gac atg tac tgc gga tagataggat gaactctgac cacaagccat 243
Ser Cys Asp Met Tyr Cys Gly
65 70

ccgacatcac cactctcctc ttcagagtct tcaag 278

<210> 33
<211> 70
<212> PRT
<213> Conus marmoreus

<400> 33
Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met Thr
1 5 10 15

Thr Gln Ala Leu Tyr Gln Glu Lys Arg Arg Lys Glu Met Ile Asn Phe
20 25 30

Leu Ser Lys Gly Lys Ile Asn Ala Glu Arg Arg Asn Gly Gly Cys Lys
35 40 45

Ala Thr Trp Met Ser Cys Ser Ser Gly Trp Glu Cys Cys Ser Met Ser
50 55 60

Cys Asp Met Tyr Cys Gly
65 70

<210> 34
<211> 528
<212> DNA
<213> Conus textile

<220>
<221> CDS
<222> (98)..(316)

<400> 34
gcacgtcatc ttctctctca gtctgcctga cagctgcctt cagtcacccc tgccgtcatc 60

tcacgcgtaga cttggtaaga agtgaaaaac atttatac atg cag aaa ctg ata atc 115
Met Gln Lys Leu Ile Ile
1 5

ctg ctt ctt gtt gct gct gtg ctg atg tcg acc cag gcc gtg ctt caa 163
Leu Leu Leu Val Ala Val Leu Met Ser Thr Gln Ala Val Leu Gln
10 15 20

gaa aaa cgc cca aag gag aag atc aag ctt tta tca aag aga aag aca 211
Glu Lys Arg Pro Lys Glu Lys Ile Lys Leu Leu Ser Lys Arg Lys Thr
25 30 35

gat gct gag aag cag cag-aag cgc ctt tgc ccg gat tac-acg gag-cct- 259
Asp Ala Glu Lys Gln Gln Lys Arg Leu Cys Pro Asp Tyr Thr Glu Pro
40 45 50

BBSTT "25607250

tgt tca cat gcc cat gaa tgc tgt tca tgg aat tgt tat aat ggg cac 307
Cys Ser His Ala His Glu Cys Cys Ser Trp Asn Cys Tyr Asn Gly His
55 60 65 70

tgt acg gga tgaactcgga ccacaagcca tccgacatca ccactctcct 356
Cys Thr Gly

cttcagaggc ttcaagactt ttgttctgat tttggacaat ctttacgagt aaacaaataa 416

ttagactagc acttttttttc ccctttgcaa aatcaatgat ggaggtaaaa agcctcccat 476

tttgtcttca tcaataaaga acttatcatc aaaaaaaaaa aaaaaaaaaa aa 528

<210> 35
<211> 73
<212> PRT
<213> Conus textile

<400> 35
Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser
1 5 10 15

Thr Gln Ala Val Leu Gln Glu Lys Arg Pro Lys Glu Lys Ile Lys Leu
20 25 30

Leu Ser Lys Arg Lys Thr Asp Ala Glu Lys Gln Gln Lys Arg Leu Cys
35 40 45

Pro Asp Tyr Thr Glu Pro Cys Ser His Ala His Glu Cys Cys Ser Trp
50 55 60

Asn Cys Tyr Asn Gly His Cys Thr Gly
65 70

<210> 36
<211> 26
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(26)
<223> Xaa at residue 18 is Trp or 6-bromo-Trp; Xaa at
residues 7 and 14 are Glu or
gamma-carboxyglutamate; Xaa at residues 3 and 8
are Pro or hydroxy-Pro.

<400> 36
Leu Cys Xaa Asp Tyr Thr Xaa Xaa Cys Ser His Ala His Xaa Cys Cys
1 5 10 15

Ser Xaa Asn Cys Tyr Asn Gly His Cys Thr
20 25

<210> 37
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus

0961095-11598

gamma-conopeptide sequence for probe

<220>
 <221> PEPTIDE
 <222> (1)
 <223> Xaa is Glu or Gln.

<400> 37
 Xaa Cys Cys Ser
 1

<210> 38
 <211> 12
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:degenerate
 probe for consensus gamma-conopeptide sequence.

<400> 38
 sartgytggya gy

12

<210> 39
 <211> 12
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:degenerate
 probe for consensus gamma-conopeptide sequence.

<400> 39
 sartgytgyt cn

12

<210> 40
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:consensus
 pro-gamma-conopeptide sequence for probe.

<400> 40
 Ile Leu Leu Val Ala Ala Val Leu
 1 5

<210> 41
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:degenerate
 probe for consensus pro-gamma-conopeptide
 sequence.

<400> 41
 athytnytng tngcngcngt nytn

24

09210952.121593

<210> 42
<211> 31
<212> PRT
<213> Conus pennaceus

<220>
<221> PEPTIDE
<222> (1)..(31)
<223> Xaa at residues 14 and 26 are
gamma-carboxyglutamate; Xaa at residue 31 is
hdroxy-Pro.

<400> 42
Asp Cys Thr Ser Trp Phe Gly Arg Cys Thr Val Asn Ser Xaa Cys Cys
1 5 10 15
Ser Asn Ser Cys Asp Gln Thr Tyr Cys Xaa Leu Tyr Ala Phe Xaa Ser
20 25 30

<210> 43
<211> 27
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa at residues 9 and 13 are
gamma-carboxyglutamate.

<400> 43
Cys Gly Gly Tyr Ser Thr Tyr Cys Xaa Val Asp Ser Xaa Cys Cys Ser
1 5 10 15
Asp Asn Cys Val Arg Ser Tyr Cys Thr Leu Phe
20 25

<210> 44
<211> 8
<212> PRT
<213> Conus pennaceus

<220>
<221> MOD_RES
<222> (2)
<223> Xaa at residue 2 is carboxymethylCys

<400> 44
Asp Xaa Thr Ser Trp Phe Gly Arg
1 5

<210> 45
<211> 24
<212> PRT
<213> Conus pennaceus

<220>
<221> PEPTIDE
<222> (1)..(24)
<223> Xaa at residues 6 and 18 are

0921055.121598

gamma-carboxyglutamate; Xaa at residue 23 is
hydroxy-Pro.

<400> 45

Xaa Thr Val Asn Ser Xaa Xaa Xaa Ser Asn Ser Xaa Asp Gln Thr Tyr
1 5 10 15

Xaa Xaa Leu Tyr Ala Phe Xaa Ser
20

<210> 46

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for M13
universal priming site.

<400> 46

tttcccagtc acgacgtt

18

<210> 47

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for M13
reverse priming site.

<400> 47

cacacaggaa acagctatg

19

09210952-12198